

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BECKMANN, M. P.  
CERRETTI, DOUGLAS P.
- (ii) TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
RECEPTOR HEK
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: IMMUNEX CORPORATION  
(B) STREET: 51 UNIVERSITY STREET  
(C) CITY: SEATTLE  
(D) STATE: WASHINGTON  
(E) COUNTRY: USA  
(F) ZIP: 98101
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: Apple Macintosh  
(C) OPERATING SYSTEM: Apple System 7.1  
(D) SOFTWARE: Microsoft Word for Apple, Version 5.1a
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/161,132  
(B) FILING DATE: 03-DEC-1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/114,426  
(B) FILING DATE: 30-AUG-1993
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/109,745  
(B) FILING DATE: 20-AUG-1993
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: SEESE, KATHRYN A.  
(B) REGISTRATION NUMBER: 32,172  
(C) REFERENCE/DOCKET NUMBER: 2814-C
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (206) 587-0430  
(B) TELEFAX: (206) 233-0644  
(C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1037 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: hek-L A2

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 83..799

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 83..139

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 140..796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATCTTGA ACGAGACGAC CTGCTGGAGA AGCCGGGAGC GCGGGGCTCA GTCGGGGGGC	60
GGCGGCGGCG GCGGCTCCGG GG ATG GCG GCG GCT CCG CTG CTG CTG CTG CTG	112
Met Ala Ala Ala Pro Leu Leu Leu Leu Leu	
-19 -15 -10	
CTG CTC GTG CCC GTG CCG CTG CTG CCG CTG CTG GCC CAA GGG CCC GGA	160
Leu Leu Val Pro Val Pro Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly	
-5 1 5	
GGG GCG CTG GGA AAC CGG CAT GCG GTG TAC TGG AAC AGC TCC AAC CAG	208
Gly Ala Leu Gly Asn Arg His Ala Val Tyr Trp Asn Ser Ser Asn Gln	
10 15 20	
CAC CTG CGG CGA GAG GGC TAC ACC GTG CAG GTG AAC GTG AAC GAC TAT	256
His Leu Arg Arg Glu Gly Tyr Thr Val Gln Val Asn Val Asn Asp Tyr	
25 30 35	
CTG GAT ATT TAC TGC CCG CAC TAC AAC AGC TCG GGG GTG GGC CCC GGG	304
Leu Asp Ile Tyr Cys Pro His Tyr Asn Ser Ser Gly Val Gly Pro Gly	
40 45 50 55	
GCG GGA CCG GGG CCC GGA GGC GGG GCA GAG CAG TAC GTG CTG TAC ATG	352
Ala Gly Pro Gly Pro Gly Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met	
60 65 70	

15640660

TCF 20 4567890

GTG AGC CGC AAC GGC TAC CGC ACC TGC AAC GCC AGC CAG GGC TTC AAG Val Ser Arg Asn Gly Tyr Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys 75 80 85	400
CGC TGG GAG TGC AAC CGG CCG CAC GCC CCG CAC AGC CCC ATC AAG TTC Arg Trp Glu Cys Asn Arg Pro His Ala Pro His Ser Pro Ile Lys Phe 90 95 100	448
TCG GAG AAG TTC CAG CGC TAC AGC GCC TTC TCT CTG GGC TAC GAG TTC Ser Glu Lys Phe Gln Arg Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe 105 110 115	496
CAC GCC GGC CAC GAG TAC TAC TAC ATC TCC ACG CCC ACT CAC AAC CTG His Ala Gly His Glu Tyr Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu 120 125 130 135	544
CAC TGG AAG TGT CTG AGG ATG AAG GTG TTC GTC TGC TGC GCC TCC ACA His Trp Lys Cys Leu Arg Met Lys Val Phe Val Cys Cys Ala Ser Thr 140 145 150	592
TCG CAC TCC GGG GAG AAG CCG GTC CCC ACT CTC CCC CAG TTC ACC ATG Ser His Ser Gly Glu Lys Pro Val Pro Thr Leu Pro Gln Phe Thr Met 155 160 165	640
GGC CCC AAT GTG AAG ATC AAC GTG CTG GAA GAC TTT GAG GGA GAG AAC Gly Pro Asn Val Lys Ile Asn Val Leu Glu Asp Phe Glu Gly Glu Asn 170 175 180	688
CCT CAG GTG CCC AAG CTT GAG AAG AGC ATC AGC GGG ACC AGC CCC AAA Pro Gln Val Pro Lys Leu Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys 185 190 195	736
CGG GAA CAC CTG CCC CTG GCC GTG GGC ATC GCC TTC TTC CTC ATG ACG Arg Glu His Leu Pro Leu Ala Val Gly Ile Ala Phe Phe Leu Met Thr 200 205 210 215	784
TTC TTG GCC TCC TAGCTCTGCC CCCTCCCCTG EGGGGGGAGA GATGGGGCGG Phe Leu Ala Ser 220	836
GGCTTGAAG GAGCAGGGAG CCTTTGGCCT CTCCAAGGGA AGCCTAGTGG GCCTAGACCC	896
CTCCTCCCAT GGCTAGAAGT GGGGCCTGCA CCATACATCT GTGTCCGCCC CCTCTACCCC	956
TTCCCCCACC GTAGGGCACT GTAGTGGACC AAGCACGGGG ACAGCCATGG GTCCCGAGCA	1016
GGTCGTCTCG TTCCAAGATC C	1037

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 238 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Ala Pro Leu Leu Leu Leu Leu Leu Val Pro Val Pro  
-19 -15 -10 -5

Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly Gly Ala Leu Gly Asn Arg  
1 5 10

His Ala Val Tyr Trp Asn Ser Ser Asn Gln His Leu Arg Arg Glu Gly  
15 20 25

Tyr Thr Val Gln Val Asn Val Asn Asp Tyr Leu Asp Ile Tyr Cys Pro  
30 35 40 45

His Tyr Asn Ser Ser Gly Val Gly Pro Gly Ala Gly Pro Gly Pro Gly  
50 55 60

Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met Val Ser Arg Asn Gly Tyr  
65 70 75

Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys Arg Trp Glu Cys Asn Arg  
80 85 90

Pro His Ala Pro His Ser Pro Ile Lys Phe Ser Glu Lys Phe Gln Arg  
95 100 105

Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe His Ala Gly His Glu Tyr  
110 115 120 125

Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu His Trp Lys Cys Leu Arg  
130 135 140

Met Lys Val Phe Val Cys Cys Ala Ser Thr Ser His Ser Gly Glu Lys  
145 150 155

Pro Val Pro Thr Leu Pro Gln Phe Thr Met Gly Pro Asn Val Lys Ile  
160 165 170

Asn Val Leu Glu Asp Phe Glu Gly Glu Asn Pro Gln Val Pro Lys Leu  
175 180 185

Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys Arg Glu His Leu Pro Leu  
190 195 200 205

Ala Val Gly Ile Ala Phe Phe Leu Met Thr Phe Leu Ala Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 636 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

CCF0450000

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: hek-L C6

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 94..630

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 28..633

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 28..93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCAGACCAA ACCGGACCTC GGGGGCG ATG CGG CTG CTG CCC CTG CTG CGG	51
Met Arg Leu Leu Pro Leu Leu Arg	
-22 -20 -15	
ACT GTC CTC TGG GCC GCG TTC CTC GGC TCC CCT CTG CGC GGG GGC TCC	99
Thr Val Leu Trp Ala Ala Phe Leu Gly Ser Pro Leu Arg Gly Gly Ser	
-10 -5 1	
AGC CTC CGC CAC GTA GTC TAC TGG AAC TCC AGT AAC CCC AGG TTG CTT	147
Ser Leu Arg His Val Val Tyr Trp Asn Ser Ser Asn Pro Arg Leu Leu	
5 10 15	
CGA GGA GAC GCC GTG GTG GAG CTG GGC CTC AAC GAT TAC CTA GAC ATT	195
Arg Gly Asp Ala Val Val Glu Leu Gly Leu Asn Asp Tyr Leu Asp Ile	
20 25 30	
GTC TGC CCC CAC TAC GAA GGC CCA GGG CCC CCT GAG GGC CCC GAG ACG	243
Val Cys Pro His Tyr Glu Gly Pro Gly Pro Pro Glu Gly Pro Glu Thr	
35 40 45 50	
TTT GCT TTG TAC ATG GTG GAC TGG CCA GGC TAT GAG TCC TGC CAG GCA	291
Phe Ala Leu Tyr Met Val Asp Trp Pro Gly Tyr Glu Ser Cys Gln Ala	
55 60 65	
GAG GGC CCC CGG GCC TAC AAG CGC TGG GTG TGC TCC CTG CCC TTT GGC	339
Glu Gly Pro Arg Ala Tyr Lys Arg Trp Val Cys Ser Leu Pro Phe Gly	
70 75 80	
CAT GTT CAA TTC TCA GAG AAG ATT CAG CGC TTC ACA CCT TTC TCC CTC	387
His Val Gln Phe Ser Glu Lys Ile Gln Arg Phe Thr Pro Phe Ser Leu	
85 90 95	
GGC TTT GAG TTC TTA CCT GGA GAG ACT TAC TAC TAC ATC TCG GTG CCC	435
Gly Phe Glu Phe Leu Pro Gly Glu Thr Tyr Tyr Tyr Ile Ser Val Pro	
100 105 110	
ACT CCA GAG AGT TCT GGC CAG TGC TTG AGG CTC CAG GTG TCT GTC TGC	483
Thr Pro Glu Ser Ser Gly Gln Cys Leu Arg Leu Gln Val Ser Val Cys	
115 120 125 130	

CCCTCGTGGGCG

TGC AAG GAG AGG AAG TCT GAG TCA GCC CAT CCT GTT GGG AGC CCT GGA	531
Cys Lys Glu Arg Lys Ser Glu Ser Ala His Pro Val Gly Ser Pro Gly	
135 140 145	
GAG AGT GGC ACA TCA GGG TGG CGA GGG GGG GAC ACT CCC AGC CCC CTC	579
Glu Ser Gly Thr Ser Gly Trp Arg Gly Gly Asp Thr Pro Ser Pro Leu	
150 155 160	
TGT CTC TTG CTA TTA CTG CTG CTT CTG ATT CTT CGT CTT CTG CGA ATT	627
Cys Leu Leu Leu Leu Leu Leu Leu Leu Ile Leu Arg Leu Leu Arg Ile	
165 170 175	
CTG TGAGCC	636
Leu	
180	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Leu Leu Pro Leu Leu Arg Thr Val Leu Trp Ala Ala Phe Leu	
-22 -20 -15 -10	
Gly Ser Pro Leu Arg Gly Gly Ser Ser Leu Arg His Val Val Tyr Trp	
-5 1 5 10	
Asn Ser Ser Asn Pro Arg Leu Leu Arg Gly Asp Ala Val Val Glu Leu	
15 20 25	
Gly Leu Asn Asp Tyr Leu Asp Ile Val Cys Pro His Tyr Glu Gly Pro	
30 35 40	
Gly Pro Pro Glu Gly Pro Glu Thr Phe Ala Leu Tyr Met Val Asp Trp	
45 50 55	
Pro Gly Tyr Glu Ser Cys Gln Ala Glu Gly Pro Arg Ala Tyr Lys Arg	
60 65 70	
Trp Val Cys Ser Leu Pro Phe Gly His Val Gln Phe Ser Glu Lys Ile	
75 80 85 90	
Gln Arg Phe Thr Pro Phe Ser Leu Gly Phe Glu Phe Leu Pro Gly Glu	
95 100 105	
Thr Tyr Tyr Tyr Ile Ser Val Pro Thr Pro Glu Ser Ser Gly Gln Cys	
110 115 120	
Leu Arg Leu Gln Val Ser Val Cys Cys Lys Glu Arg Lys Ser Glu Ser	
125 130 135	

REF ID: A56466

Ala His Pro Val Gly Ser Pro Gly Glu Ser Gly Thr Ser Gly Trp Arg  
140 145 150

Gly Gly Asp Thr Pro Ser Pro Leu Cys Leu Leu Leu Leu Leu Leu  
155 160 165 170

Leu Ile Leu Arg Leu Leu Arg Ile Leu  
175

FOR THE